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1600

RAW SEQUENCE LISTING

DATE: 12/19/2002

PATENT APPLICATION: US/09/868,987A

TIME: 13:59:59

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\12192002\I868987A.raw

4 <110> APPLICANT: Aventis Pasteur Limited
6 <120> TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
8 <130> FILE REFERENCE: 77813-73
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/868,987A
C--> 11 <141> CURRENT FILING DATE: 2001-10-01
13 <150> PRIOR APPLICATION NUMBER: 60/113,280
14 <151> PRIOR FILING DATE: 1998-12-23
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19 <150> PRIOR APPLICATION NUMBER: 60/113,282
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29 <151> PRIOR FILING DATE: 1998-12-23
31 <150> PRIOR APPLICATION NUMBER: 60/113,385
32 <151> PRIOR FILING DATE: 1998-12-23
34 <150> PRIOR APPLICATION NUMBER: 60/114,050
35 <151> PRIOR FILING DATE: 1998-12-28
37 <150> PRIOR APPLICATION NUMBER: 60/114,056
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41 <151> PRIOR FILING DATE: 1998-12-28
43 <150> PRIOR APPLICATION NUMBER: 60/114,058
44 <151> PRIOR FILING DATE: 1998-12-28
46 <150> PRIOR APPLICATION NUMBER: 60/114,059
47 <151> PRIOR FILING DATE: 1998-12-28
49 <150> PRIOR APPLICATION NUMBER: 60/114,061
50 <151> PRIOR FILING DATE: 1998-12-28
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54 <170> SOFTWARE: PatentIn Ver. 2.0
56 <210> SEQ ID NO: 1
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59 <212> TYPE: DNA
60 <213> ORGANISM: Chlamydia pneumoniae
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63 <221> NAME/KEY: CDS
64 <222> LOCATION: (101)..(1756)
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69 aaaccgtgga tggcgtatgg ctgtagtgtat tgacggttat atg gtc agc agc cct 115

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75					10					15					20		
77	acc	cac	cgt	gaa	gtg	agc	aaa	ctc	gcc	tca	gat	tta	aaa	tct	gga	gcg	211
78	Thr	His	Arg	Glu	Val	Ser	Lys	Leu	Ala	Ser	Asp	Leu	Lys	Ser	Gly	Ala	
79				25				30						35			
81	atg	tct	ttt	gtt	ccc	gag	gtt	ctc	agt	gaa	gag	acg	atc	tct	tct	gat	259
82	Met	Ser	Phe	Val	Pro	Glu	Val	Leu	Ser	Glu	Glu	Thr	Ile	Ser	Ser	Asp	
83			40					45				50					
85	ctt	ggg	aaa	aaa	caa	tgt	aca	caa	ggc	att	atc	tca	gca	tgc	tgt	ggc	307
86	Leu	Gly	Lys	Lys	Gln	Cys	Thr	Gln	Gly	Ile	Ile	Ser	Ala	Cys	Cys	Gly	
87		55					60			65							
89	ttg	gca	atg	ctt	att	gtt	ttg	atg	agc	gta	tat	tat	aga	ttt	gga	ggc	355
90	Leu	Ala	Met	Leu	Ile	Val	Leu	Met	Ser	Val	Tyr	Tyr	Arg	Phe	Gly	Gly	
91	70				75					80					85		
93	gtc	atc	gct	tcg	gga	gct	gtt	ctt	ctg	aat	ctt	ttg	ctt	atc	tgg	gca	403
94	Val	Ile	Ala	Ser	Gly	Ala	Val	Leu	Leu	Asn	Leu	Leu	Leu	Ile	Trp	Ala	
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97	gct	cta	cag	tat	ttg	gat	gcg	cca	ctc	acc	ttg	tca	gga	ctc	gct	ggg	451
98	Ala	Leu	Gln	Tyr	Leu	Asp	Ala	Pro	Leu	Thr	Leu	Ser	Gly	Leu	Ala	Gly	
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103			120				125					130					
105	gaa	aga	atc	cga	gag	gaa	ttt	tta	ttg	tct	caa	agt	ctt	aaa	aaa	tct	547
106	Glu	Arg	Ile	Arg	Glu	Glu	Phe	Leu	Leu	Ser	Gln	Ser	Leu	Lys	Lys	Ser	
107		135				140				145							
109	gta	gaa	aaa	gga	tat	acc	aag	gct	ttt	gga	gcc	att	ttt	gat	tct	aac	595
110	Val	Glu	Lys	Gly	Tyr	Thr	Lys	Ala	Phe	Gly	Ala	Ile	Phe	Asp	Ser	Asn	
111	150				155			160							165		
113	ttg	act	aca	gta	ttg	gcc	tca	gca	ctt	ctt	ttc	ttc	cta	gat	aca	ggg	643
114	Leu	Thr	Thr	Val	Leu	Ala	Ser	Ala	Leu	Leu	Phe	Phe	Leu	Asp	Thr	Gly	
115			170				175				180						
117	cct	att	aaa	ggg	ttt	gct	ttg	aca	ttg	att	tta	gga	att	ttc	tct	tca	691
118	Pro	Ile	Lys	Gly	Phe	Ala	Leu	Thr	Leu	Ile	Leu	Gly	Ile	Phe	Ser	Ser	
119			185				190				195						
121	atg	ttt	acg	gct	ctt	ttc	atg	act	aaa	ttt	ttc	ttc	atg	ctg	tgg	atg	739
122	Met	Phe	Thr	Ala	Leu	Phe	Met	Thr	Lys	Phe	Phe	Phe	Met	Leu	Trp	Met	
123			200				205				210						
125	aat	aag	acc	caa	cat	aca	cag	ttg	cat	atg	atg	aat	aag	ttc	gtg	ggg	787
126	Asn	Lys	Thr	Gln	His	Thr	Gln	Leu	His	Met	Met	Asn	Lys	Phe	Val	Gly	
127		215				220					225						
129	ata	aag	cat	gat	ttc	ttg	aga	gga	tgc	aaa	aaa	ctt	tgg	gct	gtt	tct	835
130	Ile	Lys	His	Asp	Phe	Leu	Arg	Gly	Cys	Lys	Lys	Leu	Trp	Ala	Val	Ser	
131	230				235			240						245			
133	gga	agt	gtt	ttt	ctt	tta	ggg	tgc	gtt	gct	ctc	ggg	ttt	gga	gcc	tgg	883
134	Gly	Ser	Val	Phe	Leu	Leu	Gly	Cys	Val	Ala	Leu	Gly	Phe	Gly	Ala	Trp	

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137	aat tcc gtt ttg gga atg gat ttt aaa gga ggg tat gcc ttt acc ttt							931
138	Asn Ser Val Leu Gly Met Asp Phe Lys Gly Gly Tyr Ala Phe Thr Phe							
139		265		270		275		
141	aat cca aaa gag cat ggc atc agc gat gtt gct caa atg cgt ggc aaa							979
142	Asn Pro Lys Glu His Gly Ile Ser Asp Val Ala Gln Met Arg Gly Lys							
143		280		285		290		
145	gtt gtg cat aaa cta cag gaa gct ggt ctt tct tct aga gac ttc cgt							1027
146	Val Val His Lys Leu Gln Glu Ala Gly Leu Ser Ser Arg Asp Phe Arg							
147		295		300		305		
149	att caa aca ttt gga tct tca gaa aag atc aaa atc tat ttt agt gat							1075
150	Ile Gln Thr Phe Gly Ser Ser Glu Lys Ile Lys Ile Tyr Phe Ser Asp							
151	310		315		320		325	
153	aaa gct tta agc tat act aag cag ata cga gcc tct ctc cta aaa tta							1123
154	Lys Ala Leu Ser Tyr Thr Lys Gln Ile Arg Ala Ser Leu Leu Lys Leu							
155		330		335		340		
157	acg atc atg agc tgg cgt tat tgt ggg att gtt gtc aga aac agg cct							1171
158	Thr Ile Met Ser Trp Arg Tyr Cys Gly Ile Val Val Arg Asn Arg Pro							
159		345		350		355		
161	aga ttt ctc tac gga aac tct aaa cga aac gca aaa ttt tgg tca aag							1219
162	Arg Phe Leu Tyr Gly Asn Ser Lys Arg Asn Ala Lys Phe Trp Ser Lys							
163		360		365		370		
165	gta agc agc aaa cta tcg aag aaa atg cgt tat cag gcg acc atc ggg							1267
166	Val Ser Ser Lys Leu Ser Lys Lys Met Arg Tyr Gln Ala Thr Ile Gly							
167		375		380		385		
169	ctt tta gga gct ttg gca atc atc ttg ctc tat gtg agt ttg cgc ttt							1315
170	Leu Leu Gly Ala Leu Ala Ile Ile Leu Leu Tyr Val Ser Leu Arg Phe							
171	390		395		400		405	
175	gaa tgg caa tat gct ttc agt gcc gta tgc gct tta att cat gac ctt							1363
176	Glu Trp Gln Tyr Ala Phe Ser Ala Val Cys Ala Leu Ile His Asp Leu							
177		410		415		420		
179	ttg gct acc tgt gca gtc ttg ttt ata gca cat ttc ttt ttg aag aaa							1411
180	Leu Ala Thr Cys Ala Val Leu Phe Ile Ala His Phe Phe Leu Lys Lys							
181		425		430		435		
183	att caa ata gat ttg caa gcc att ggt gct tta atg act gta ttg ggg							1459
184	Ile Gln Ile Asp Leu Gln Ala Ile Gly Ala Leu Met Thr Val Leu Gly							
185		440		445		450		
187	tat tca tta aac aat act ttg atc att ttt gat cgt att cgt gaa gat							1507
188	Tyr Ser Leu Asn Asn Thr Leu Ile Ile Phe Asp Arg Ile Arg Glu Asp							
189		455		460		465		
191	cgc caa gcg aac ctg ttt acc cct atg cat gtt tta gtt aat gat gcc							1555
192	Arg Gln Ala Asn Leu Phe Thr Pro Met His Val Leu Val Asn Asp Ala							
193	470		475		480		485	
195	ctt caa aag acg ttc agc cgc acg gta atg aca aca gct aca act cta							1603
196	Leu Gln Lys Thr Ser Arg Thr Val Met Thr Thr Ala Thr Thr Leu							
197		490		495		500		
199	tca gtt ttg tta atg ctt ttg ttt ata ggc ggc tcc tct gtc ttt aat							1651
200	Ser Val Leu Leu Met Leu Leu Phe Ile Gly Gly Ser Ser Val Phe Asn							
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207 ctt tat att gca cca cct ctg ttg ttg ttt atg gtc cgt aaa gaa aat 1747
208 Leu Tyr Ile Ala Pro Pro Leu Leu Leu Phe Met Val Arg Lys Glu Asn
209          535          540          545
211 cgc tca aaa taagtaccgt taaacttaat ctaacgtgta gcaatataaa 1796
212 Arg Ser Lys
213 550
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225 <222> LOCATION: (101)..(688)
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231 Met Ser Ser Asn Leu
232          1          5
233 cat ccc gta gga gga aca gga aca gga gca gct gct cct gag tct gtg 163
234 His Pro Val Gly Gly Thr Gly Thr Gly Ala Ala Ala Pro Glu Ser Val
235          10          15          20
237 cta aac ata gta gag gaa ata gca gca tcg ggg agt gtc acc gct ggt 211
238 Leu Asn Ile Val Glu Glu Ile Ala Ala Ser Gly Ser Val Thr Ala Gly
239          25          30          35
241 cta caa gca att acg tcc agt cca gga atg gtg aat cta ctc ata gga 259
242 Leu Gln Ala Ile Thr Ser Ser Pro Gly Met Val Asn Leu Leu Ile Gly
243          40          45          50
245 tgg gca aag aca aaa ttt att caa cct ata cgt gaa tca aag ctc ttt 307
246 Trp Ala Lys Thr Lys Phe Ile Gln Pro Ile Arg Glu Ser Lys Leu Phe
247          55          60          65
249 caa tcc aga gct tgc caa att acc ctg ctc gtt tta gga att ctt ttg 355
250 Gln Ser Arg Ala Cys Gln Ile Thr Leu Leu Val Leu Gly Ile Leu Leu
251 70          75          80          85
253 gtt gtt gct gga tta gca tgt atg ttt atc ttc cat agc cag tta ggg 403
254 Val Val Ala Gly Leu Ala Cys Met Phe Ile Phe His Ser Gln Leu Gly
255          90          95          100
257 gca aat gca ttt tgg ttg att att cct gct gcc ata gga ttg att aag 451
258 Ala Asn Ala Phe Trp Leu Ile Ile Pro Ala Ala Ile Gly Leu Ile Lys
259          105          110          115
261 tta cta gtt aca tca tta tgt ttt gat gaa gct tgt aca tct gaa aaa 499
262 Leu Leu Val Thr Ser Leu Cys Phe Asp Glu Ala Cys Thr Ser Glu Lys
263          120          125          130
265 ctc atg gtt ttc caa aaa tgg gca ggt gtt tta gaa gat cag ctc gat 547
266 Leu Met Val Phe Gln Lys Trp Ala Gly Val Leu Glu Asp Gln Leu Asp

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271 150      155      160      165
273 gaa gga aat acc tct agg gct act acc cca gta ctt aat gat ggc cgc 643
274 Glu Gly Asn Thr Ser Arg Ala Thr Thr Pro Val Leu Asn Asp Gly Arg
275      170      175      180
277 gga act cct gta ctt tca cct tta gta agt aaa ata gct cgc gtt 688
278 Gly Thr Pro Val Leu Ser Pro Leu Val Ser Lys Ile Ala Arg Val
279      185      190      195
281 tagacgttca tctcacaagc atcctagaac ttgggatgct actttccacg tacgagatca 748
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285 <211> LENGTH: 950
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287 <213> ORGANISM: Chlamydia pneumoniae
291 <220> FEATURE:
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299 Met Thr Ile Arg Ile
300      1      5
302 ctt gct gaa ggc cta gct ttc cgt tac gga agc aag gga ccg aat atc 163
303 Leu Ala Glu Gly Leu Ala Phe Arg Tyr Gly Ser Lys Gly Pro Asn Ile
304      10      15      20
306 att cat gat gtt tct ttc tct gtc tat gat ggc gac ttt ata gga atc 211
307 Ile His Asp Val Ser Phe Ser Val Tyr Asp Gly Asp Phe Ile Gly Ile
308      25      30      35
310 ata gga cca aac gga ggg ggg aaa agc acc tta acg atg tta att ttg 259
311 Ile Gly Pro Asn Gly Gly Gly Lys Ser Thr Leu Thr Met Leu Ile Leu
312      40      45      50
314 ggc ttg ctt act cct aca ttc gga tcc ttg aag act ttc cct tcg cat 307
315 Gly Leu Leu Thr Pro Thr Phe Gly Ser Leu Lys Thr Phe Pro Ser His
316      55      60      65
318 tcc gcg ggg aaa caa acc cat tcc atg atc ggt tgg gtt ccc caa cat 355
319 Ser Ala Gly Lys Gln Thr His Ser Met Ile Gly Trp Val Pro Gln His
320      70      75      80      85
322 ttc tct tat gat cct tgt ttt cct atc tca gta aaa gat gtt gtc ctc 403
323 Phe Ser Tyr Asp Pro Cys Phe Pro Ile Ser Val Lys Asp Val Val Leu
324      90      95      100
326 tca gga aga ttg tct caa ctc tcc tgg cat gga aaa tat aaa aag aaa 451
327 Ser Gly Arg Leu Ser Gln Leu Ser Trp His Gly Lys Tyr Lys Lys Lys
328      105      110      115
330 gat ttt gaa gct gta gat cac gct ttg gat ctt gtt gga ctt tct gac 499
331 Asp Phe Glu Ala Val Asp His Ala Leu Asp Leu Val Gly Leu Ser Asp
332      120      125      130
334 acc acc acc act gct ttc gcc cat ctc tca gga gga caa atc cag cgt 547

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 1254,1266,1323